RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/526,650

Source: PCT

Date Processed by STIC: 3-13-08

ENTERED

PCT

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RAW SEQUENCE LISTING              DATE: 03/13/2005
PATENT APPLICATION:  US/10/526,650   TIME: 12:13:01

Input Set : A:\seqlist.txt
Output Set: N:\CRF4\03132005\J526650.raw
```

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    4 <110> APPLICANT: Kobayashi, Masanori
    5        Ueda, Yasuji
    6        Hasegawa, Mamoru
    8 <120> TITLE OF INVENTION: Methods of Producing a Viral Vector
    9        Comprising a Membrane Protein That Binds To Sialic Acid As A
   10        Component Of The Envelope Using Neuraminidase Derived From
   11        Gram-Positive Bacteria
   14 <130> FILE REFERENCE: 50026/050001
C--> 16 <140> CURRENT APPLICATION NUMBER: US/10/526,650
C--> 16 <141> CURRENT FILING DATE: 2005-03-03
   16 <150> PRIOR APPLICATION NUMBER: PCT/JP03/11299
   17 <151> PRIOR FILING DATE: 2003-09-04
   19 <150> PRIOR APPLICATION NUMBER: JP 2002-258576
   20 <151> PRIOR FILING DATE: 2002-09-04
   22 <160> NUMBER OF SEQ ID NOS: 2
   24 <170> SOFTWARE: FastSEQ for Windows Version 4.0
   26 <210> SEQ ID NO: 1
   27 <211> LENGTH: 1941
   28 <212> TYPE: DNA
   29 <213> ORGANISM: Micromonospora viridifaciens
   31 <220> FEATURE:
   32 <221> NAME/KEY: CDS
   33 <222> LOCATION: (1)...(1941)
   35 <400> SEQUENCE: 1
   36 atg act gcg aat ccg tac ctc cgc cgc ctg ccc cgg cgc cga gcc gtc    48
   37 Met Thr Ala Asn Pro Tyr Leu Arg Arg Leu Pro Arg Arg Arg Ala Val
   38 1               5                   10                  15
   40 agc ttc ctg ctc gca cca gcg ctg gcg gcc gcc acg gtc gcc ggc gcg    96
   41 Ser Phe Leu Leu Ala Pro Ala Leu Ala Ala Ala Thr Val Ala Gly Ala
   42             20                  25                  30
   44 tcc ccc gca cag gcc atc gcc ggg gca ccc gtc ccg ccc ggc ggc gag   144
   45 Ser Pro Ala Gln Ala Ile Ala Gly Ala Pro Val Pro Pro Gly Gly Glu
   46         35                  40                  45
   48 ccg ctc tac acg gag cag gac ctc gcc gtg aac ggc agg gag ggc ttt   192
   49 Pro Leu Tyr Thr Glu Gln Asp Leu Ala Val Asn Gly Arg Glu Gly Phe
   50     50                  55                  60
   52 ccg aac tac cgc atc cca gcg ctg acc gtc acg ccc gac ggg gac ctg   240
   53 Pro Asn Tyr Arg Ile Pro Ala Leu Thr Val Thr Pro Asp Gly Asp Leu
   54 65                  70                  75                  80
   56 ctg gcc tcg tac gac ggc cgc ccg acc ggt atc gac gcg ccc ggc ccc   288
   57 Leu Ala Ser Tyr Asp Gly Arg Pro Thr Gly Ile Asp Ala Pro Gly Pro
   58             85                  90                  95
   60 aac tcc atc ctc caa cgc cgc agc acc gac ggc ggc cgg acg tgg ggc   336
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```
61 Asn Ser Ile Leu Gln Arg Arg Ser Thr Asp Gly Gly Arg Thr Trp Gly
62              100                 105                 110
64 gag caa cag gtc gtc agc gcc ggc cag acc acc gcg ccg atc aag ggg   384
65 Glu Gln Gln Val Val Ser Ala Gly Gln Thr Thr Ala Pro Ile Lys Gly
66              115                 120                 125
68 ttc tcc gac ccc agc tac ctt gtc gac cgg gaa acc ggg acc atc ttc   432
69 Phe Ser Asp Pro Ser Tyr Leu Val Asp Arg Glu Thr Gly Thr Ile Phe
70        130                 135                 140
72 aac ttc cac gtc tac tcc cag cgg cag ggc ttc gcc ggc agc cgg ccc   480
73 Asn Phe His Val Tyr Ser Gln Arg Gln Gly Phe Ala Gly Ser Arg Pro
74 145                 150                 155                 160
76 ggc acc gac ccg gca gac ccc aac gtg ctc cac gcc aac gtc gcg acc   528
77 Gly Thr Asp Pro Ala Asp Pro Asn Val Leu His Ala Asn Val Ala Thr
78              165                 170                 175
80 tcg acc gac ggc ggt ctg acc tgg tcg cac cgg acc atc acg gcc gac   576
81 Ser Thr Asp Gly Gly Leu Thr Trp Ser His Arg Thr Ile Thr Ala Asp
82              180                 185                 190
84 atc acc ccg gat ccg ggc tgg cgc agc cgc ttc gcc gcc tcc ggc gaa   624
85 Ile Thr Pro Asp Pro Gly Trp Arg Ser Arg Phe Ala Ala Ser Gly Glu
86              195                 200                 205
88 ggc atc cag ctc cgc tat gga ccc cac gcc ggt cga ctc atc cag cag   672
89 Gly Ile Gln Leu Arg Tyr Gly Pro His Ala Gly Arg Leu Ile Gln Gln
90        210                 215                 220
92 tac acg atc atc aac gct gcc ggc gcc ttc cag gcg gtg agc gtg tac   720
93 Tyr Thr Ile Ile Asn Ala Ala Gly Ala Phe Gln Ala Val Ser Val Tyr
94 225                 230                 235                 240
96 agc gac gac cac gga agg acc tgg cgc gcc ggc gaa gcc gtc ggg gtc   768
97 Ser Asp Asp His Gly Arg Thr Trp Arg Ala Gly Glu Ala Val Gly Val
98              245                 250                 255
100 ggc atg gac gag aac aag acc gtg gaa ctc tcc gat ggc cgg gtc ctg   816
101 Gly Met Asp Glu Asn Lys Thr Val Glu Leu Ser Asp Gly Arg Val Leu
102             260                 265                 270
104 ctc aac agc cgc gac tcg gcc cgc agc gga tac cgt aag gtg gcc gtc   864
105 Leu Asn Ser Arg Asp Ser Ala Arg Ser Gly Tyr Arg Lys Val Ala Val
106             275                 280                 285
108 tcc act gac ggc ggc cac agc tac ggc ccg gtg acc atc gac cgc gac   912
109 Ser Thr Asp Gly Gly His Ser Tyr Gly Pro Val Thr Ile Asp Arg Asp
110       290                 295                 300
112 ctc ccc gac ccg acg aac aac gca tcg atc atc cgg gcc ttc cct gac   960
113 Leu Pro Asp Pro Thr Asn Asn Ala Ser Ile Ile Arg Ala Phe Pro Asp
114 305                 310                 315                 320
116 gcc ccg gcc ggc tcc gcg cgg gcc aag gtc ctg ctc ttc tcc aac gcc   1008
117 Ala Pro Ala Gly Ser Ala Arg Ala Lys Val Leu Leu Phe Ser Asn Ala
118             325                 330                 335
120 gcc agc cag acc tcg cgc agt cag ggc acc atc cgg atg tcc tgc gac   1056
121 Ala Ser Gln Thr Ser Arg Ser Gln Gly Thr Ile Arg Met Ser Cys Asp
122             340                 345                 350
124 gat ggc cag acc tgg ccg gtt tcg aag gtc ttc cag ccc ggc tcg atg   1104
125 Asp Gly Gln Thr Trp Pro Val Ser Lys Val Phe Gln Pro Gly Ser Met
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126        355              360              365
128 tcg tac tcc acc ctg acc gca ctg ccc gac ggc acc tac ggg ctg ctg   1152
129 Ser Tyr Ser Thr Leu Thr Ala Leu Pro Asp Gly Thr Tyr Gly Leu Leu
130        370              375              380
132 tac gag ccg ggc acc ggc atc aga tac gcc aac ttc aac ctc gcc tgg   1200
133 Tyr Glu Pro Gly Thr Gly Ile Arg Tyr Ala Asn Phe Asn Leu Ala Trp
134 385              390              395              400
136 ctg ggc ggc atc tgc gcg ccc ttc acg att ccg gat gtg gcg ctc gag   1248
137 Leu Gly Gly Ile Cys Ala Pro Phe Thr Ile Pro Asp Val Ala Leu Glu
138        405              410              415
140 ccg ggc cag cag gtc act gtt ccg gtg gcc gtc acg aac cag tcc ggt   1296
141 Pro Gly Gln Gln Val Thr Val Pro Val Ala Val Thr Asn Gln Ser Gly
142        420              425              430
144 atc gcg gta ccg aag ccg agc ctt cag ctc gac gca tcg ccg gac tgg   1344
145 Ile Ala Val Pro Lys Pro Ser Leu Gln Leu Asp Ala Ser Pro Asp Trp
146        435              440              445
148 cag gtt cag ggt tcc gtc gag ccc ctc atg ccc gga cgg cag gcc aag   1392
149 Gln Val Gln Gly Ser Val Glu Pro Leu Met Pro Gly Arg Gln Ala Lys
150        450              455              460
152 ggc cag gtg acc atc acg gtt ccc gcc ggc acc acc ccc ggt cgc tac   1440
153 Gly Gln Val Thr Ile Thr Val Pro Ala Gly Thr Thr Pro Gly Arg Tyr
154 465              470              475              480
156 cgg gtc ggt gcg acg ctg cgc acc tcc gcg ggt aac gcg tcg acg acc   1488
157 Arg Val Gly Ala Thr Leu Arg Thr Ser Ala Gly Asn Ala Ser Thr Thr
158        485              490              495
160 ttc acg gtc acg gtt gga ctg ctc gac cag gcc cgg atg agc atc gcg   1536
161 Phe Thr Val Thr Val Gly Leu Leu Asp Gln Ala Arg Met Ser Ile Ala
162        500              505              510
164 gac gtc gac agc gag gag acc gcc cgc gaa gac ggg cgg gcg agc aac   1584
165 Asp Val Asp Ser Glu Glu Thr Ala Arg Glu Asp Gly Arg Ala Ser Asn
166        515              520              525
168 gtg atc gac ggc aac ccc tcg acg ttc tgg cac acc gaa tgg tcg cgt   1632
169 Val Ile Asp Gly Asn Pro Ser Thr Phe Trp His Thr Glu Trp Ser Arg
170        530              535              540
172 gcc gat gct cct ggc tac ccg cac cgc atc agc ctc gac ctc ggt ggc   1680
173 Ala Asp Ala Pro Gly Tyr Pro His Arg Ile Ser Leu Asp Leu Gly Gly
174 545              550              555              560
176 acg cac acg atc agc ggc ctc cag tac acc cga cgg cag aac agc gcc   1728
177 Thr His Thr Ile Ser Gly Leu Gln Tyr Thr Arg Arg Gln Asn Ser Ala
178        565              570              575
180 aac gag cag gtc gcg gac tac gag atc tac acc agc ctg aac ggc acg   1776
181 Asn Glu Gln Val Ala Asp Tyr Glu Ile Tyr Thr Ser Leu Asn Gly Thr
182        580              585              590
184 acc tgg gat ggc ccg gtt gcc agc ggg cgc ttc acc acg tcc ctc gcg   1824
185 Thr Trp Asp Gly Pro Val Ala Ser Gly Arg Phe Thr Thr Ser Leu Ala
186        595              600              605
188 ccg cag cgc gcg gtc ttc ccg gcg cgg gac gcc agg tac atc cgg ttg   1872
189 Pro Gln Arg Ala Val Phe Pro Ala Arg Asp Ala Arg Tyr Ile Arg Leu
190        610              615              620
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RAW SEQUENCE LISTING   DATE: 03/13/2005
PATENT APPLICATION: US/10/526,650   TIME: 12:13:01

Input Set : **A:\seqlist.txt**
Output Set: **N:\CRF4\03132005\J526650.raw**

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192 gtg gcc ctc agc gag cag acc ggg cac aag tac gcc gcg gtc gct gag    1920
193 Val Ala Leu Ser Glu Gln Thr Gly His Lys Tyr Ala Ala Val Ala Glu
194 625             630             635             640
196 ctg gag gtg gaa ggc cag cgc                                        1941
197 Leu Glu Val Glu Gly Gln Arg
198             645
201 <210> SEQ ID NO: 2
202 <211> LENGTH: 647
203 <212> TYPE: PRT
204 <213> ORGANISM: Micromonospora viridifaciens
206 <400> SEQUENCE: 2
207 Met Thr Ala Asn Pro Tyr Leu Arg Arg Leu Pro Arg Arg Arg Ala Val
208 1               5               10              15
209 Ser Phe Leu Leu Ala Pro Ala Leu Ala Ala Ala Thr Val Ala Gly Ala
210             20              25              30
211 Ser Pro Ala Gln Ala Ile Ala Gly Ala Pro Val Pro Pro Gly Gly Glu
212         35              40              45
213 Pro Leu Tyr Thr Glu Gln Asp Leu Ala Val Asn Gly Arg Glu Gly Phe
214     50              55              60
215 Pro Asn Tyr Arg Ile Pro Ala Leu Thr Val Thr Pro Asp Gly Asp Leu
216 65              70              75              80
217 Leu Ala Ser Tyr Asp Gly Arg Pro Thr Gly Ile Asp Ala Pro Gly Pro
218             85              90              95
219 Asn Ser Ile Leu Gln Arg Arg Ser Thr Asp Gly Gly Arg Thr Trp Gly
220             100             105             110
221 Glu Gln Gln Val Val Ser Ala Gly Gln Thr Thr Ala Pro Ile Lys Gly
222         115             120             125
223 Phe Ser Asp Pro Ser Tyr Leu Val Asp Arg Glu Thr Gly Thr Ile Phe
224     130             135             140
225 Asn Phe His Val Tyr Ser Gln Arg Gln Gly Phe Ala Gly Ser Arg Pro
226 145             150             155             160
227 Gly Thr Asp Pro Ala Asp Pro Asn Val Leu His Ala Asn Val Ala Thr
228             165             170             175
229 Ser Thr Asp Gly Gly Leu Thr Trp Ser His Arg Thr Ile Thr Ala Asp
230             180             185             190
231 Ile Thr Pro Asp Pro Gly Trp Arg Ser Arg Phe Ala Ala Ser Gly Glu
232         195             200             205
233 Gly Ile Gln Leu Arg Tyr Gly Pro His Ala Gly Arg Leu Ile Gln Gln
234     210             215             220
235 Tyr Thr Ile Ile Asn Ala Ala Gly Ala Phe Gln Ala Val Ser Val Tyr
236 225             230             235             240
237 Ser Asp Asp His Gly Arg Thr Trp Arg Ala Gly Glu Ala Val Gly Val
238             245             250             255
239 Gly Met Asp Glu Asn Lys Thr Val Glu Leu Ser Asp Gly Arg Val Leu
240             260             265             270
241 Leu Asn Ser Arg Asp Ser Ala Arg Ser Gly Tyr Arg Lys Val Ala Val
242         275             280             285
243 Ser Thr Asp Gly Gly His Ser Tyr Gly Pro Val Thr Ile Asp Arg Asp
244         290             295             300
```

```
245 Leu Pro Asp Pro Thr Asn Asn Ala Ser Ile Ile Arg Ala Phe Pro Asp
246 305                 310                 315                 320
247 Ala Pro Ala Gly Ser Ala Arg Ala Lys Val Leu Leu Phe Ser Asn Ala
248                 325                 330                 335
249 Ala Ser Gln Thr Ser Arg Ser Gln Gly Thr Ile Arg Met Ser Cys Asp
250                 340                 345 ·               350
251 Asp Gly Gln Thr Trp Pro Val Ser Lys Val Phe Gln Pro Gly Ser Met
252         355                 360                 365
253 Ser Tyr Ser Thr Leu Thr Ala Leu Pro Asp Gly Thr Tyr Gly Leu Leu
254         370                 375                 380
255 Tyr Glu Pro Gly Thr Gly Ile Arg Tyr Ala Asn Phe Asn Leu Ala Trp
256 385                 390                 395                 400
257 Leu Gly Gly Ile Cys Ala Pro Phe Thr Ile Pro Asp Val Ala Leu Glu
258                 405                 410                 415
259 Pro Gly Gln Gln Val Thr Val Pro Val Ala Val Thr Asn Gln Ser Gly
260                 420                 425                 430
261 Ile Ala Val Pro Lys Pro Ser Leu Gln Leu Asp Ala Ser Pro Asp Trp
262         435                 440                 445
263 Gln Val Gln Gly Ser Val Glu Pro Leu Met Pro Gly Arg Gln Ala Lys
264         450                 455                 460
265 Gly Gln Val Thr Ile Thr Val Pro Ala Gly Thr Thr Pro Gly Arg Tyr
266 465                 470                 475                 480
267 Arg Val Gly Ala Thr Leu Arg Thr Ser Ala Gly Asn Ala Ser Thr Thr
268                 485                 490                 495
269 Phe Thr Val Thr Val Gly Leu Leu Asp Gln Ala Arg Met Ser Ile Ala
270                 500                 505                 510
271 Asp Val Asp Ser Glu Glu Thr Ala Arg Glu Asp Gly Arg Ala Ser Asn
272         515                 520                 525
273 Val Ile Asp Gly Asn Pro Ser Thr Phe Trp His Thr Glu Trp Ser Arg
274         530                 535                 540
275 Ala Asp Ala Pro Gly Tyr Pro His Arg Ile Ser Leu Asp Leu Gly Gly
276 545             ⌐    550                 555                 560
277 Thr His Thr Ile Ser Gly Leu Gln Tyr Thr Arg Arg Gln Asn Ser Ala
278                 565                 570                 575
279 Asn Glu Gln Val Ala Asp Tyr Glu Ile Tyr Thr Ser Leu Asn Gly Thr
280                 580                 585                 590
281 Thr Trp Asp Gly Pro Val Ala Ser Gly Arg Phe Thr Thr Ser Leu Ala
282         595                 600                 605
283 Pro Gln Arg Ala Val Phe Pro Ala Arg Asp Ala Arg Tyr Ile Arg Leu
284         610                 615                 620
285 Val Ala Leu Ser Glu Gln Thr Gly His Lys Tyr Ala Ala Val Ala Glu
286 625                 630                 635                 640
287 Leu Glu Val Glu Gly Gln Arg
288                 645
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VERIFICATION SUMMARY   DATE: 03/13/2005
PATENT APPLICATION: **US/10/526,650**   TIME: 12:13:02

Input Set : **A:\seqlist.txt**
Output Set: **N:\CRF4\03132005\J526650.raw**

L:16 M:270 C: Current Application Number differs, Replaced Current Application No
L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date